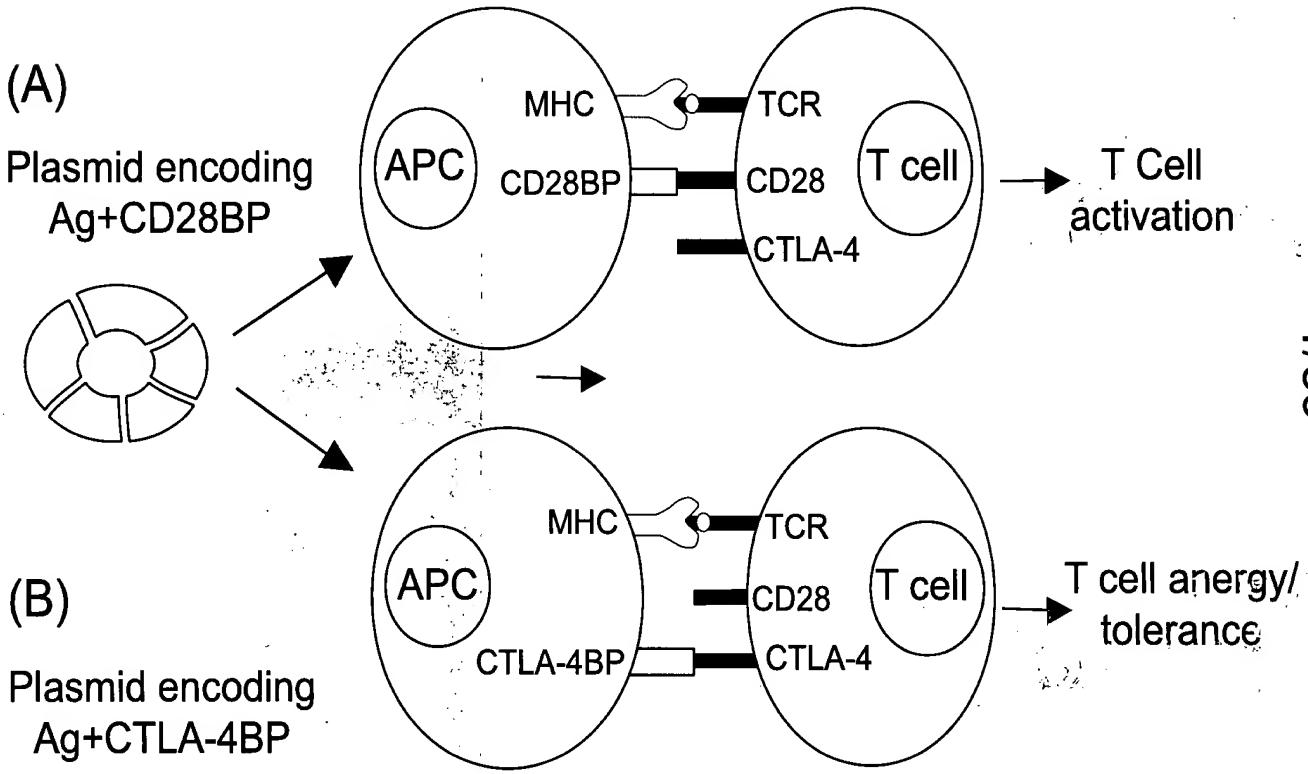
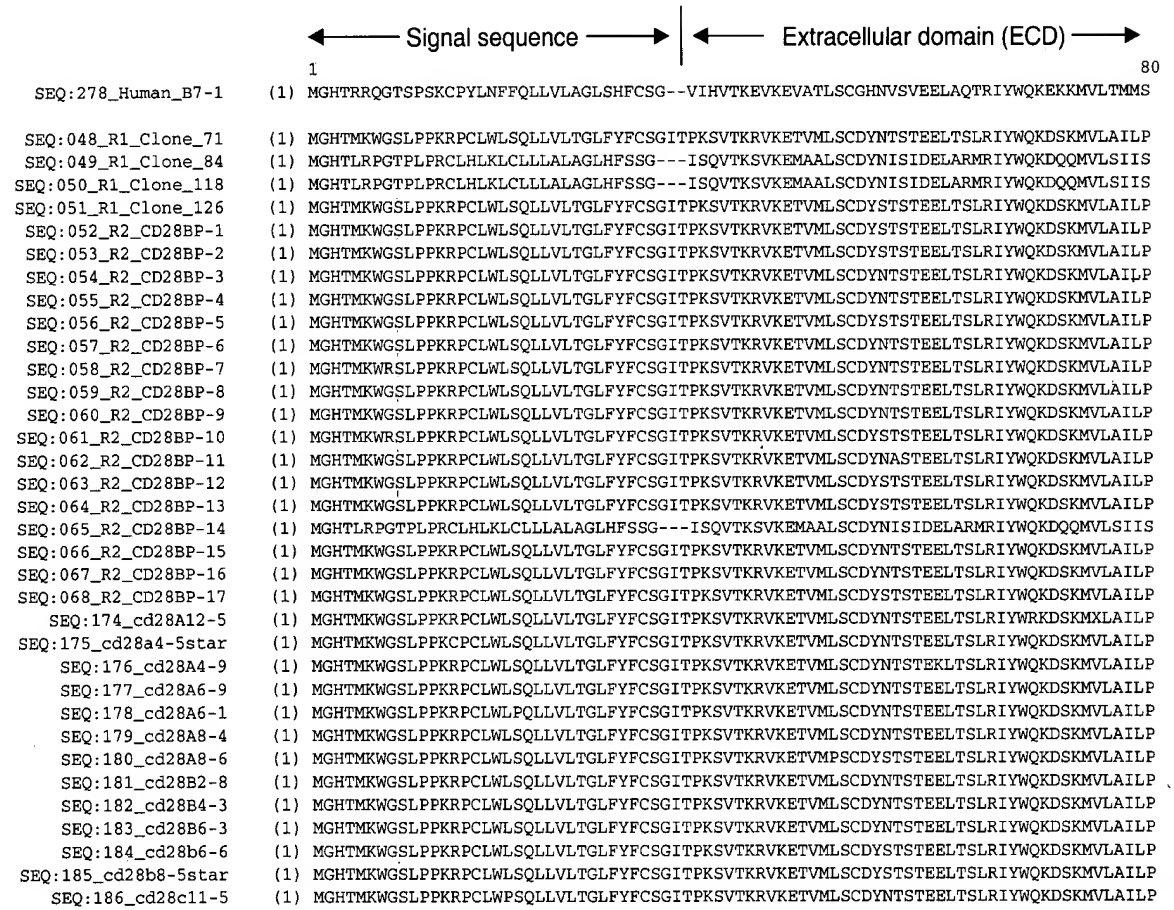

(A)
Plasmid encoding
Ag+CD28BP
APC
MHC
CD28BP
TCR
CD28
CTLA-4
T cell
T Cell
activation
(B)
Plasmid encoding
Ag+CTLA-4BP
APC
MHC
CTLA-4BP
TCR
CD28
CTLA-4
T cell
T cell anergy/
tolerance

Fig. 1


Signal sequence
Extracellular domain (ECD)
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SEQ:048_R1_Clone_71 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:049_R1_Clone_84 (1) MGHTLRPGTPLPRCLHLKLCLLLALAGLHFSSG---ISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIIS
SEQ:050_R1_Clone_118 (1) MGHTLRPGTPLPRCLHLKLCLLLALAGLHFSSG---ISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIIS
SEQ:051_R1_Clone_126 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:052_R2_CD28BP-1 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:053_R2_CD28BP-2 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:054_R2_CD28BP-3 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:055_R2_CD28BP-4 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:056_R2_CD28BP-5 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:060_R2_CD28BP-9 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:061_R2_CD28BP-10 (1) MGHTMKWRSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:062_R2_CD28BP-11 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNASTEELTSLRIYWQKDSKMVLAILP
SEQ:063_R2_CD28BP-12 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:174_cd28A12-5 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWRKDSKMXLAILP
SEQ:175_cd28a4-5star (1) MGHTMKWGSLPPKCPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:176_cd28A4-9 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEKLTSLRIYWQKDSKMVLAILP
SEQ:177_cd28A6-9 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:178_cd28A6-1 (1) MGHTMKWGSLPPKRPCLWLPQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:179_cd28A8-4 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:181_cd28B2-8 (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:185_cd28b8-5star (1) MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:186_cd28c11-5 (1) MGHTMKWGSLPPKRPCLWPSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP

Fig. 2A

←—— Signal sequence ——→ | ←—— Extracellular domain (ECD) ——→

		1 … 80
SEQ:187_cd28C6-1	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:188_cd28C7-3	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:189_cd28C8-6	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:190_cd28c9-5star	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:192_cd28D2-3	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:193_cd28D2-9	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:194_cd28D8-9	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:195_cd28D11-1	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:196_cd28D12-5	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:197_cd28E10-6	(1)	MGHTMEWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:202_cd28G2-8	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:203_cd28G1-5	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:204_cd28G1-9	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:205_cd28H4-3	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTDLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:206_cd28H11-3	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:207_cd28H6-6	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:208_cd28E2-4	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:209_cd28B4-5a	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
SEQ:210_cd28A2-5a	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:211_cd28B4-5star	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:212_cd28D5-6	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
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SEQ:216_cd28E8-6	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:217_cd28E9-6	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:218_cd28F3-1	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:219_cd28F3-5	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP
SEQ:220_cd28F3-6	(1)	MGHTMKWGSLPPKRPCLRLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKMVLAILP
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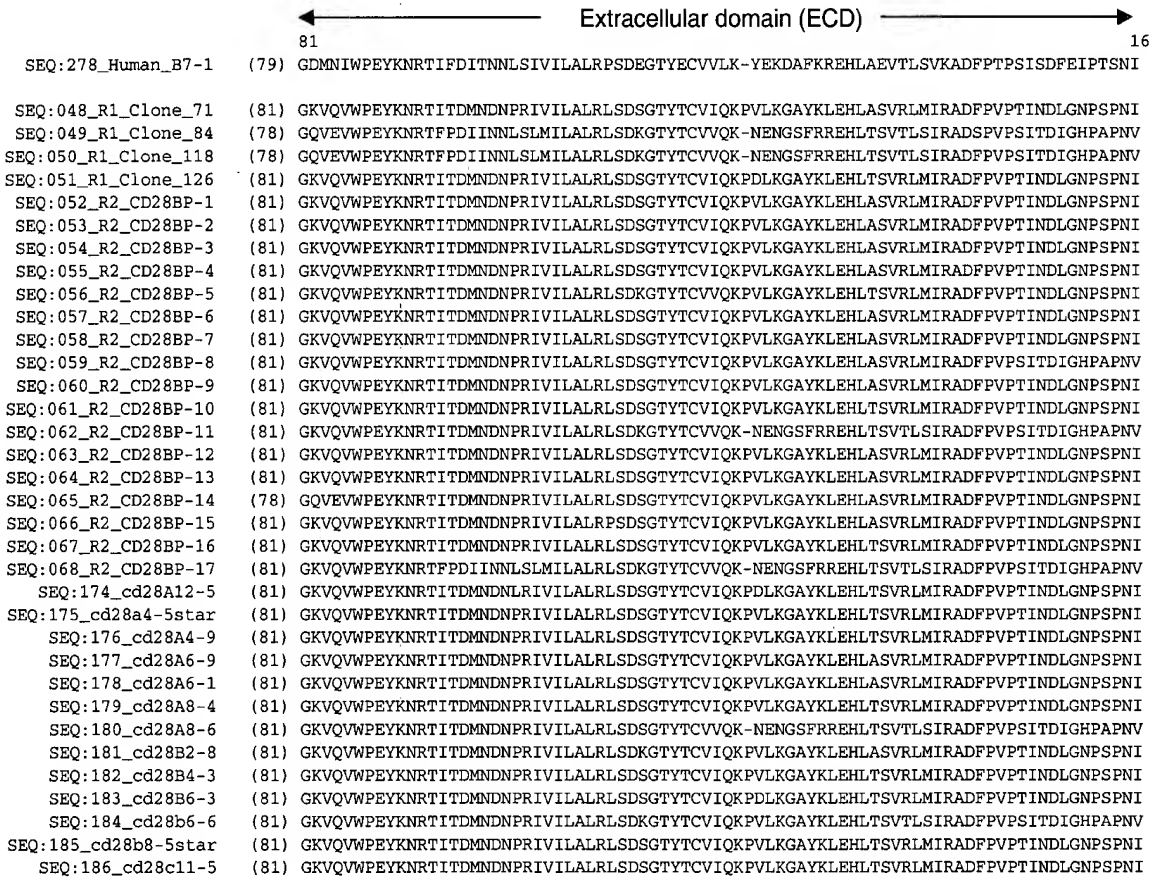
SEQ:283_CD28BP_Con	(1)	MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILP

Fig. 2B


Extracellular domain (ECD)
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SEQ:048_R1_Clone_71 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:049_R1_Clone_84 (78) GQVEVWPEYKNRTFPDIINNLSLMILALRLSDKGTYTCVVQK-NENGSFRREHLTSVTLSIRADSPVPSITDIGHPAPNV
SEQ:050_R1_Clone_118 (78) GQVEVWPEYKNRTFPDIINNLSLMILALRLSDKGTYTCVVQK-NENGSFRREHLTSVTLSIRADFPVPSITDIGHPAPNV
SEQ:051_R1_Clone_126 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:052_R2_CD28BP-1 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:053_R2_CD28BP-2 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:054_R2_CD28BP-3 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:055_R2_CD28BP-4 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:056_R2_CD28BP-5 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDKGTYTCVVQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:057_R2_CD28BP-6 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:058_R2_CD28BP-7 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:059_R2_CD28BP-8 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPSITDIGHPAPNV
SEQ:060_R2_CD28BP-9 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:061_R2_CD28BP-10 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:062_R2_CD28BP-11 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDKGTYTCVVQK-NENGSFRREHLTSVTLSIRADFPVPSITDIGHPAPNV
SEQ:063_R2_CD28BP-12 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:064_R2_CD28BP-13 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:065_R2_CD28BP-14 (78) GQVEVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:066_R2_CD28BP-15 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRPSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:067_R2_CD28BP-16 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:068_R2_CD28BP-17 (81) GKVQVWPEYKNRTFPDIINNLSLMILALRLSDKGTYTCVVQK-NENGSFRREHLTSVTLSIRADFPVPSITDIGHPAPNV
SEQ:174_cd28A12-5 (81) GKVQVWPEYKNRTITDMNDNLRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
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SEQ:176_cd28A4-9 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:177_cd28A6-9 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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SEQ:179_cd28A8-4 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
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SEQ:181_cd28B2-8 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDKGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:182_cd28B4-3 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:183_cd28B6-3 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
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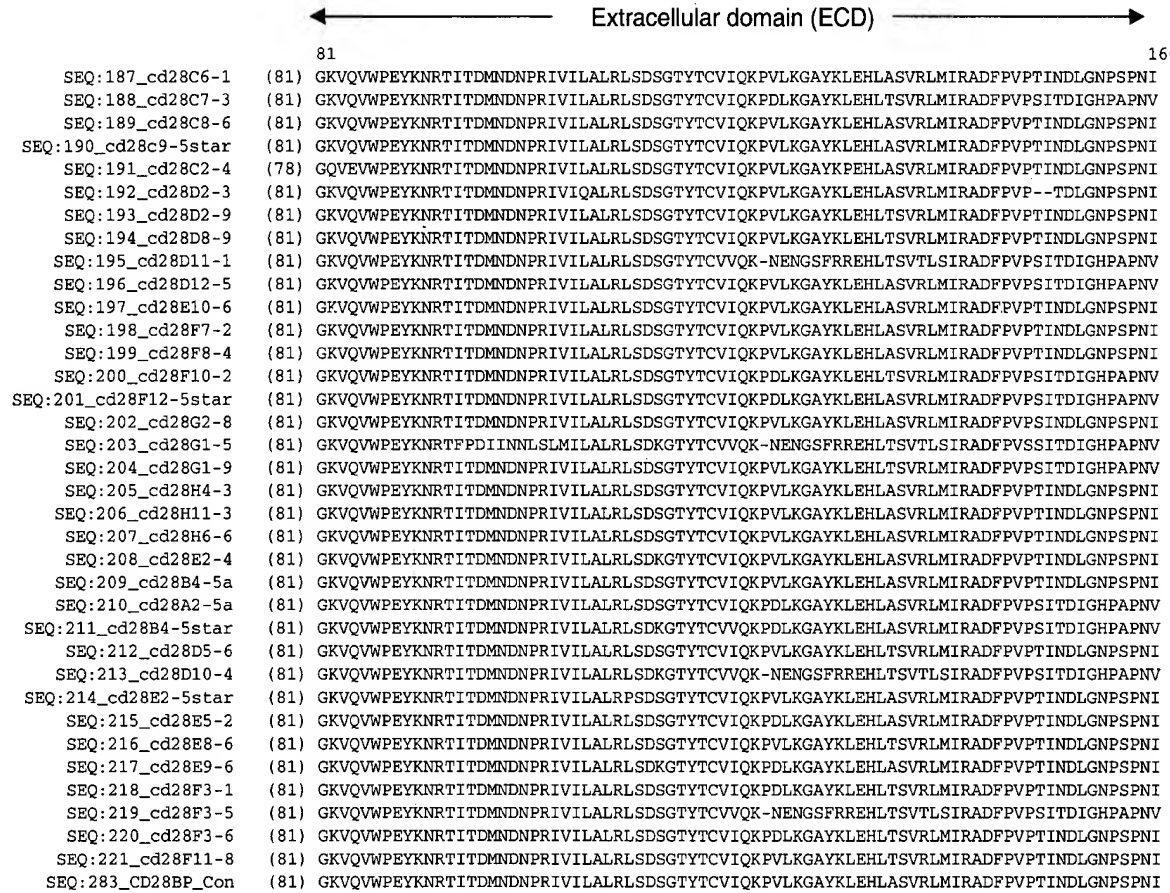
SEQ:186_cd28c11-5 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI

Fig. 2C


Extracellular domain (ECD)
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160
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SEQ:190_cd28c9-5star (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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SEQ:196_cd28D12-5 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPSITDIGHPAPNV
SEQ:197_cd28E10-6 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:198_cd28F7-2 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:199_cd28F8-4 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:200_cd28F10-2 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADFPVPSITDIGHPAPNV
SEQ:201_cd28F12-5star (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLASVRLMIRADFPVPSITDIGHPAPNV
SEQ:202_cd28G2-8 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPSINDLGNPSPNI
SEQ:203_cd28G1-5 (81) GKVQVWPEYKNRTFPDIINNLSLMILALRLSDKGTYTCVVQK-NENGSFRREHLTSVTLSIRADFPVSSITDIGHPAPNV
SEQ:204_cd28G1-9 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPSITDIGHPAPNV
SEQ:205_cd28H4-3 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:206_cd28H11-3 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:207_cd28H6-6 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:208_cd28E2-4 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDKGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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SEQ:211_cd28B4-5star (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDKGTYTCVVQKPDLKGAYKLEHLASVRLMIRADFPVPSITDIGHPAPNV
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SEQ:214_cd28E2-5star (81) GKVQVWPEYKNRTITDMNDNPRIVILALRPSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:215_cd28E5-2 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
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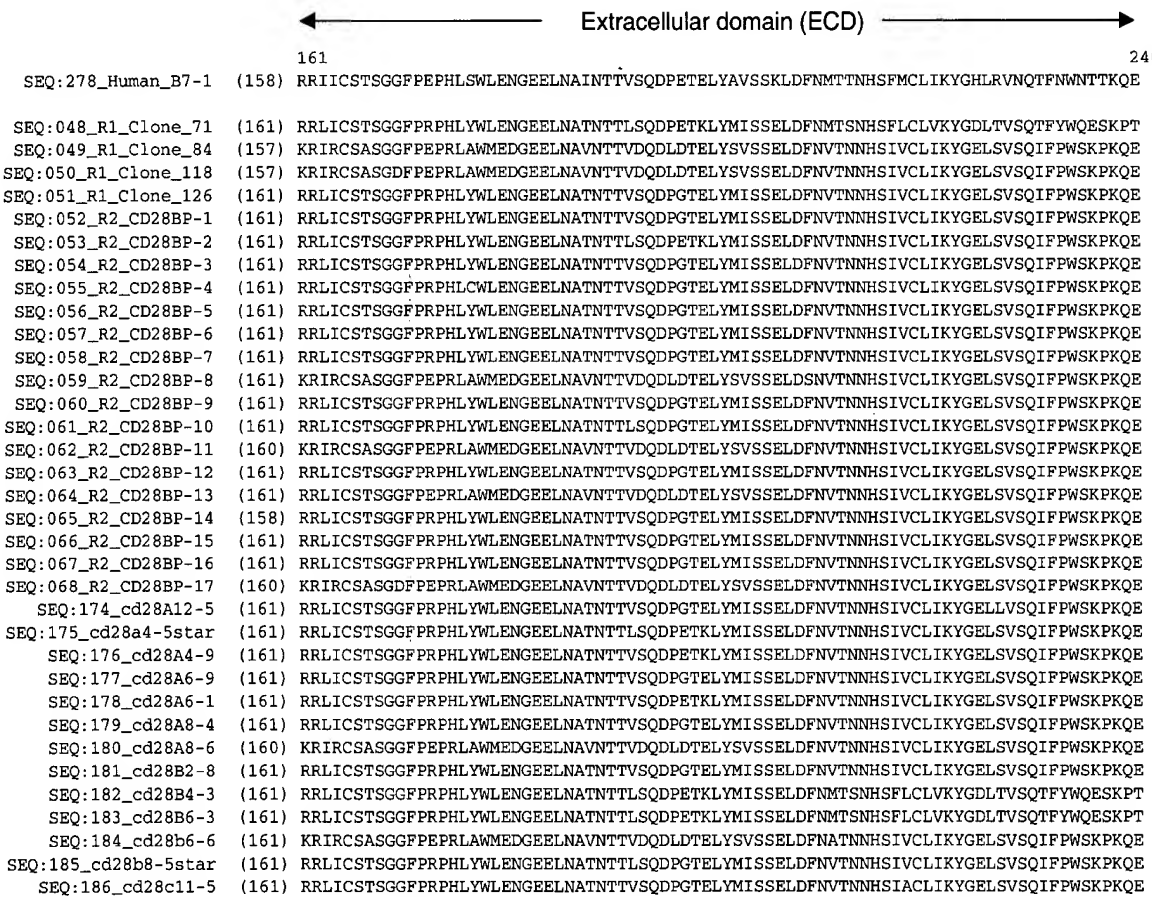
SEQ:220_cd28F3-6 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:221_cd28F11-8 (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ:283_CD28BP_Con (81) GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI

Fig. 2D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SEQ:053_R2_CD28BP-2 (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTLSQDPETKLYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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SEQ:059_R2_CD28BP-8 (161) KRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDSNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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SEQ:063_R2_CD28BP-12 (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTVSQDPGTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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SEQ:181_cd28B2-8 (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTVSQDPGTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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SEQ:185_cd28b8-5star (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTLSQDPGTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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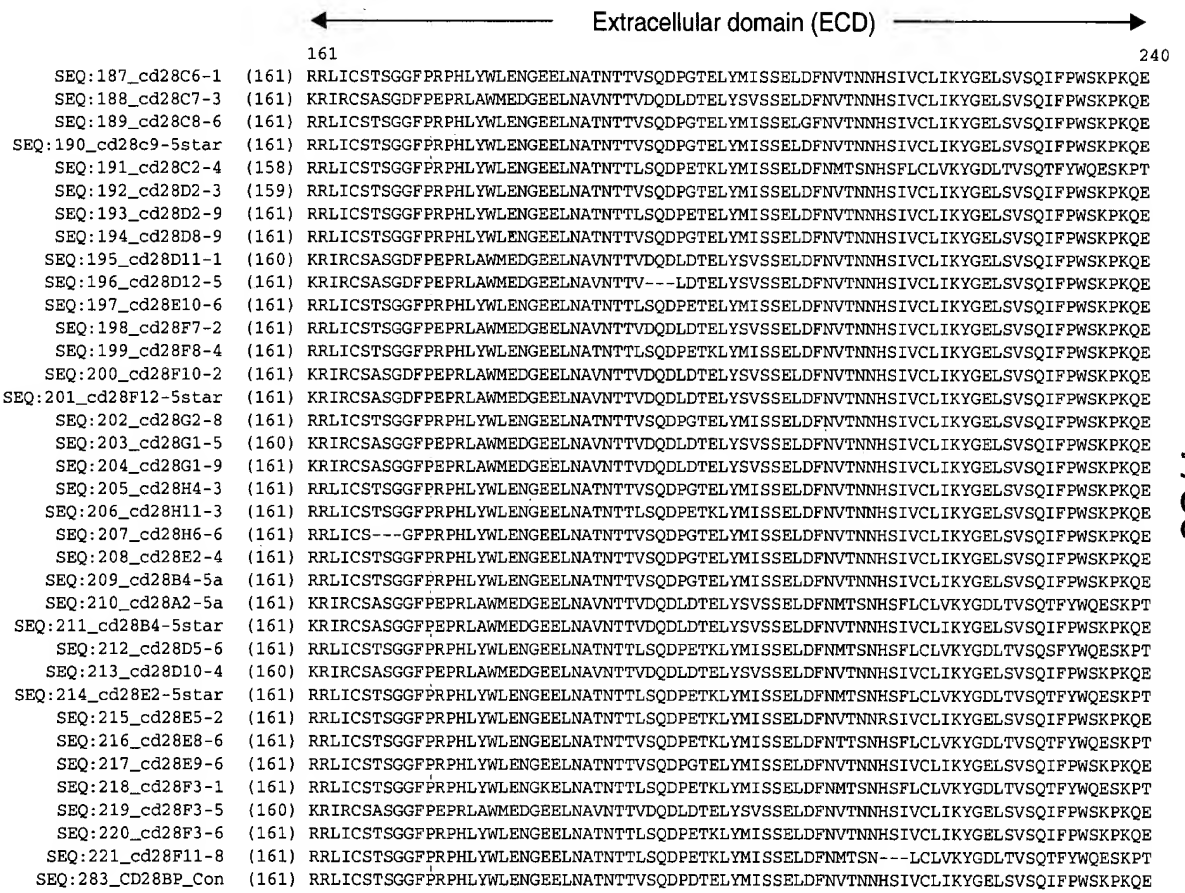
Fig. 2E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240
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SEQ:204_cd28G1-9 (161) KRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
SEQ:205_cd28H4-3 (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTVSQDPGTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE
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SEQ:283_CD28BP_Con (161) RRLICSTSGGFPRPHLYWLENGEELNATNTTVSQDPDTELYMISSELDFNVTNNHSIVCLIKYGELSVSQIFPWSKPKQE

Fig. 2F

```
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SEQ:049_R1_Clone_84   (237) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:050_R1_Clone_118  (237) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
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SEQ:068_R2_CD28BP-17  (240) P-PIDQLPFWVIIP---VSGALVLTVVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:174_cd28A12-5     (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:175_cd28a4-5star  (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:176_cd28A4-9      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCPACRHVARWKRTRRNEETVGTERLSPIYLGSAQSRAEVPSLSX
SEQ:177_cd28A6-9      (241) P-PIDQLPFLVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:178_cd28A6-1      (241) P-PIDQLPFRVIIP---VSGALVLTAIVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:179_cd28A8-4      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:180_cd28A8-6      (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:181_cd28B2-8      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:182_cd28B4-3      (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:183_cd28B6-3      (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVKMQSCSQSP----------
SEQ:184_cd28b6-6      (241) P-PIDQLPFWVIVP---VSGALVLTAVVLYCLACRHVAR---------------------------
SEQ:185_cd28b8-5star  (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:186_cd28c11-5     (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
```

Fig. 2G

```
                          ECD →|←     TMD     →|←        CD        →
                            241                                               307
SEQ:187_cd28C6-1      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHGARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:188_cd28C7-3      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:189_cd28C8-6      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:190_cd28c9-5star  (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARXKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:191_cd28C2-4      (238) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:192_cd28D2-3      (239) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:193_cd28D2-9      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:194_cd28D8-9      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:195_cd28D11-1     (240) P-PIDQLPFWVIIL---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:196_cd28D12-5     (238) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQPSG
SEQ:197_cd28E10-6     (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:198_cd28F7-2      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:199_cd28F8-4      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:200_cd28F10-2     (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:201_cd28F12-5star (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:202_cd28G2-8      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:203_cd28G1-5      (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:204_cd28G1-9      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:205_cd28H4-3      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:206_cd28H11-3     (241) P-PIDQLPFWVIIP---VSGALVLTAAVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:207_cd28H6-6      (238) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:208_cd28E2-4      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:209_cd28B4-5a     (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:210_cd28A2-5a     (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEGKCKVLSVSIGTKLKFNR--
SEQ:211_cd28B4-5star  (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:212_cd28D5-6      (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:213_cd28D10-4     (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:214_cd28E2-5star  (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:215_cd28E5-2      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:216_cd28E8-6      (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:217_cd28E9-6      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:218_cd28F3-1      (241) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:219_cd28F3-5      (240) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:220_cd28F3-6      (241) P-PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
SEQ:221_cd28F11-8     (238) P-SANQHLTWTIIIPVSAFGISVIIAVILTCLTCRNAAIRRQRRENEVEMQSCSQSP----------
SEQ:283_CD28BP_Con    (241) P PIDQLPFWVIIP---VSGALVLTAVVLYCLACRHVARWKRTRRNEETVGTERLSPIYLGSAQSSG
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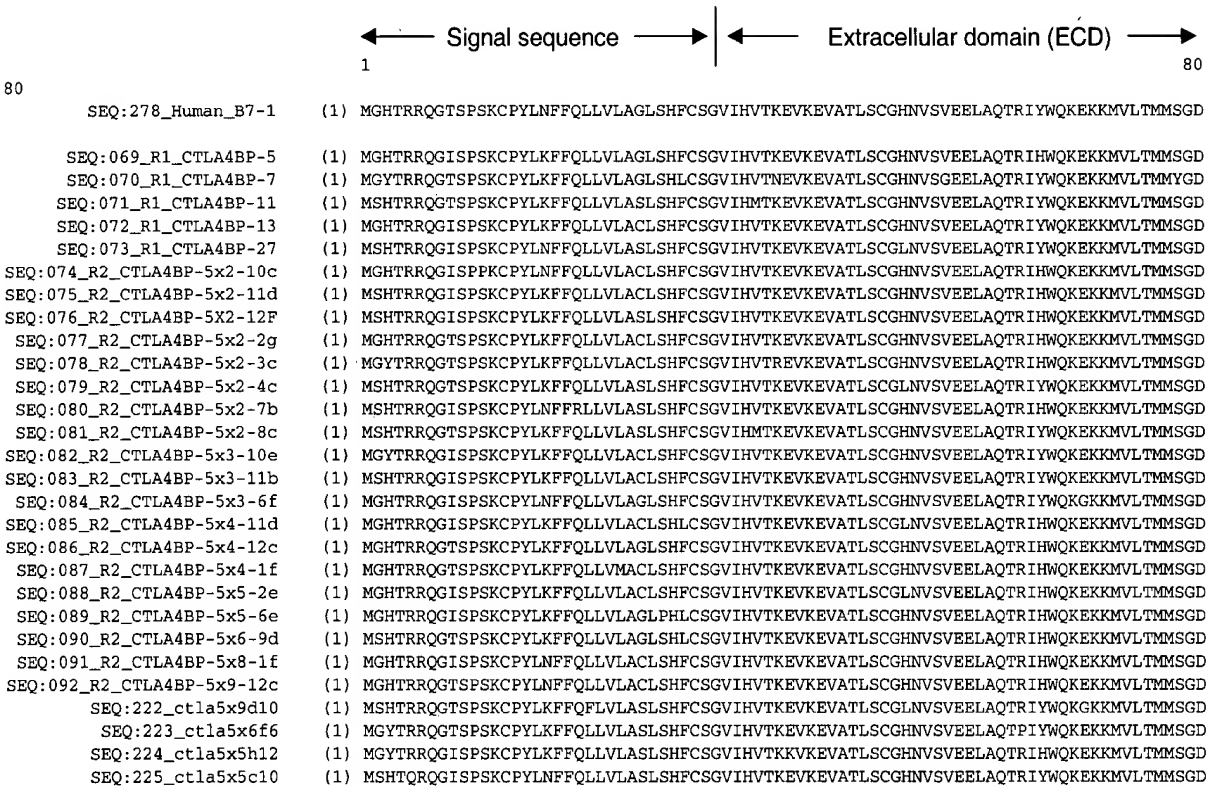
Fig. 2H


Signal sequence
Extracellular domain (ECD)
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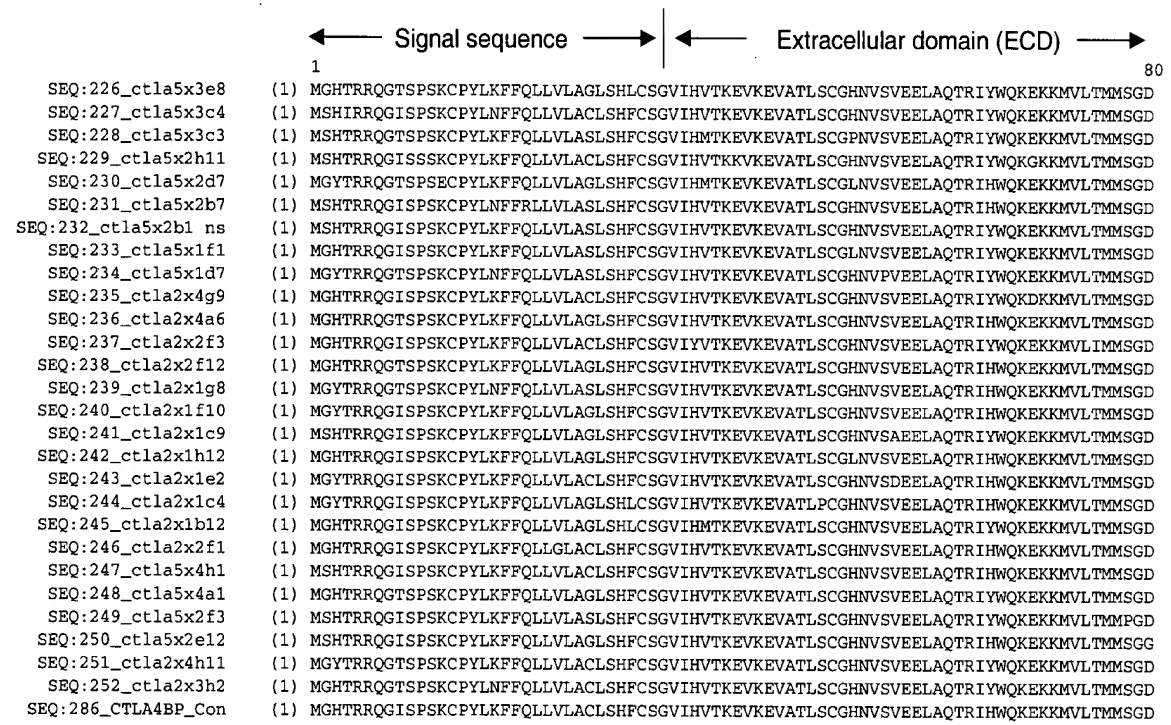
SEQ:278_Human_B7-1 (1) MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:069_R1_CTLA4BP-5 (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:070_R1_CTLA4BP-7 (1) MGYTRRQGTSPSKCPYLKFFQLLVLAGLSHLCSGVIHVTNEVKEVATLSCGHNVSGEELAQTRIYWQKEKKMVLTMMYGD
SEQ:071_R1_CTLA4BP-11 (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHMTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:072_R1_CTLA4BP-13 (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:073_R1_CTLA4BP-27 (1) MSHTRRQGISPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:074_R2_CTLA4BP-5x2-10c (1) MGHTRRQGISPPKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:075_R2_CTLA4BP-5x2-11d (1) MSHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:076_R2_CTLA4BP-5X2-12F (1) MSHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:077_R2_CTLA4BP-5x2-2g (1) MGHTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:078_R2_CTLA4BP-5x2-3c (1) MGYTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTREVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:079_R2_CTLA4BP-5x2-4c (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:080_R2_CTLA4BP-5x2-7b (1) MSHTRRQGISPSKCPYLNFFRLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:081_R2_CTLA4BP-5x2-8c (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHMTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:082_R2_CTLA4BP-5x3-10e (1) MGYTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:083_R2_CTLA4BP-5x3-11b (1) MSHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:084_R2_CTLA4BP-5x3-6f (1) MGHTRRQGISPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKGKKMVLTMMSGD
SEQ:085_R2_CTLA4BP-5x4-11d (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHLCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:086_R2_CTLA4BP-5x4-12c (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:087_R2_CTLA4BP-5x4-1f (1) MGHTRRQGTSPSKCPYLKFFQLLVMACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:088_R2_CTLA4BP-5x5-2e (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:089_R2_CTLA4BP-5x5-6e (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLPHLCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:090_R2_CTLA4BP-5x6-9d (1) MSHTRRQGTSPSKCPYLKFFQLLVLAGLSHLCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:091_R2_CTLA4BP-5x8-1f (1) MGHTRRQGISPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:092_R2_CTLA4BP-5x9-12c (1) MGHTRRQGTSPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:222_ctla5x9d10 (1) MSHTRRQGTSPSKCPYLKFFQFLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKGKKMVLTMMSGD
SEQ:223_ctla5x6f6 (1) MGYTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTPIYWQKEKKMVLTMMSGD
SEQ:224_ctla5x5h12 (1) MGYTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKKVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:225_ctla5x5c10 (1) MSHTQRQGISPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD

Fig. 3A


Signal sequence
Extracellular domain (ECD)
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SEQ:227_ctla5x3c4 (1) MSHIRRQGISPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:228_ctla5x3c3 (1) MSHTRRQGTSPSKCPYLKFFQLLVLASLSHFCSGVIHMTKEVKEVATLSCGPNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:229_ctla5x2h11 (1) MSHTRRQGISSSKCPYLKFFQLLVLACLSHFCSGVIHVTKKVKEVATLSCGHNVSVEELAQTRIYWQKGKKMVLTMMSGD
SEQ:230_ctla5x2d7 (1) MGYTRRQGTSPSECPYLKFFQLLVLAGLSHFCSGVIHMTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:231_ctla5x2b7 (1) MSHTRRQGISPSKCPYLNFFRLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:232_ctla5x2b1 ns (1) MSHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:233_ctla5x1f1 (1) MGHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:234_ctla5x1d7 (1) MGYTRRQGTSPSKCPYLNFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVPVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:235_ctla2x4g9 (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKDKKMVLTMMSGD
SEQ:236_ctla2x4a6 (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:237_ctla2x2f3 (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIYVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLIMMSGD
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SEQ:241_ctla2x1c9 (1) MSHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSAEELAQTRIYWQKEKKMVLTMMSGD
SEQ:242_ctla2x1h12 (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGLNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:243_ctla2x1e2 (1) MGYTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSDEELAQTRIHWQKEKKMVLTMMSGD
SEQ:244_ctla2x1c4 (1) MGYTRRQGISPSKCPYLKFFQLLVLAGLSHLCSGVIHVTKEVKEVATLPCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:245_ctla2x1b12 (1) MGHTRRQGISPSKCPYLKFFQLLVLAGLSHLCSGVIHMTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:246_ctla2x2f1 (1) MGHTRRQGISPSKCPYLKFFQLLGLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:247_ctla5x4h1 (1) MSHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD
SEQ:248_ctla5x4a1 (1) MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:249_ctla5x2f3 (1) MSHTRRQGISPSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMPGD
SEQ:250_ctla5x2e12 (1) MSHTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGG
SEQ:251_ctla2x4h11 (1) MGYTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:252_ctla2x3h2 (1) MGHTRRQGTSPSKCPYLNFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGD
SEQ:286_CTLA4BP_Con (1) MGHTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIHWQKEKKMVLTMMSGD

Fig. 3B

Extracellular domain (ECD)

Sequence	Start	81 … 160
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SEQ:069_R1_CTLA4BP-5	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:070_R1_CTLA4BP-7	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:071_R1_CTLA4BP-11	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:072_R1_CTLA4BP-13	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:073_R1_CTLA4BP-27	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:074_R2_CTLA4BP-5x2-10c	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:075_R2_CTLA4BP-5x2-11d	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:076_R2_CTLA4BP-5X2-12F	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIKRI
SEQ:077_R2_CTLA4BP-5x2-2g	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPTSNIRRI
SEQ:078_R2_CTLA4BP-5x2-3c	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPTSNIRRI
SEQ:079_R2_CTLA4BP-5x2-4c	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:080_R2_CTLA4BP-5x2-7b	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKAGFPTPSITDFEIPPSNIRRI
SEQ:081_R2_CTLA4BP-5x2-8c	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKQEHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:082_R2_CTLA4BP-5x3-10e	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:083_R2_CTLA4BP-5x3-11b	(81)	MNIWPEYKNRTIFDITNNLSIVILALRSSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIRRI
SEQ:084_R2_CTLA4BP-5x3-6f	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPTSNIRRI
SEQ:085_R2_CTLA4BP-5x4-11d	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYDKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:086_R2_CTLA4BP-5x4-12c	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:087_R2_CTLA4BP-5x4-1f	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPTSNIRRI
SEQ:088_R2_CTLA4BP-5x5-2e	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:089_R2_CTLA4BP-5x5-6e	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:090_R2_CTLA4BP-5x6-9d	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPTSNIRRI
SEQ:091_R2_CTLA4BP-5x8-1f	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:092_R2_CTLA4BP-5x9-12c	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:222_ctla5x9d10	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:223_ctla5x6f6	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:224_ctla5x5h12	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:225_ctla5x5c10	(81)	MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIRRI

Fig. 3C

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                                  Extracellular domain (ECD)
                      81                                                                            160
SEQ:226_ctla5x3e8    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:227_ctla5x3c4    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:228_ctla5x3c3    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:229_ctla5x2h11   (81) MNIWPECKNRTIFDITNNLSIVILALRPSDEGTYECAVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:230_ctla5x2d7    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:231_ctla5x2b7    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIRRI
SEQ:232_ctla5x2b1 ns (81) MNIWPEHKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:233_ctla5x1f1    (81) MNIWPEHKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIRRI
SEQ:234_ctla5x1d7    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYGCVVLEYEKDAFKREHLAEVMLSVKADFPTPSITDLEIPPSNIRRI
SEQ:235_ctla2x4g9    (81) MNIWPEYKNQTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKQEHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:236_ctla2x4a6    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:237_ctla2x2f3    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGT-ECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:238_ctla2x2f12   (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYGCVVLEYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:239_ctla2x1g8    (81) MNIWPEYKNRTIFDITNNLSVVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPPSNIRRI
SEQ:240_ctla2x1f10   (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:241_ctla2x1c9    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPTSNIRRI
SEQ:242_ctla2x1h12   (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:243_ctla2x1e2    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:244_ctla2x1c4    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSITDFEIPPSNIRRI
SEQ:245_ctla2x1b12   (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVALKYEKDAFKQEHLAEVTLSVKADFPTPSISDFEIPPSNIRRI
SEQ:246_ctla2x2f1    (81) MNIWPEYKNRTIFDITNNLSIVILALRLSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:247_ctla5x4h1    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKRKHLAEVMLSVKADFPTPSISDFEIPTSNIRRI
SEQ:248_ctla5x4a1    (81) MNIWPEHKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSITDFEIPTSNIRRI
SEQ:249_ctla5x2f3    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLRYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:250_ctla5x2e12   (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
SEQ:251_ctla2x4h11   (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLEYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:252_ctla2x3h2    (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
SEQ:286_CTLA4BP_Con  (81) MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSISDFEIPPSNIRRI
```

Fig. 3D

Extracellular domain (ECD)

		161 ... 240
SEQ:278_Human_B7-1	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP
SEQ:069_R1_CTLA4BP-5	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:070_R1_CTLA4BP-7	(161)	ICLTSGGFPEPRLAWMKDGEELNAISTTVSQDPGTELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFSWNTPKQEHFP
SEQ:071_R1_CTLA4BP-11	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP
SEQ:072_R1_CTLA4BP-13	(161)	ICSTSGGFPEPHLFGLENGEEINAINTTASQDPETELYTVSSKLDFNMTPNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:073_R1_CTLA4BP-27	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:074_R2_CTLA4BP-5x2-10c	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:075_R2_CTLA4BP-5x2-11d	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTDRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:076_R2_CTLA4BP-5X2-12F	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:077_R2_CTLA4BP-5x2-2g	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:078_R2_CTLA4BP-5x2-3c	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETGLYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:079_R2_CTLA4BP-5x2-4c	(161)	ICSTSGGFPEPHLSWLENGEELNGINTTVSQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:080_R2_CTLA4BP-5x2-7b	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:081_R2_CTLA4BP-5x2-8c	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:082_R2_CTLA4BP-5x3-10e	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:083_R2_CTLA4BP-5x3-11b	(161)	ICSTSGGFPEPHLSWLENGEELNAISTTVSQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:084_R2_CTLA4BP-5x3-6f	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTASQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:085_R2_CTLA4BP-5x4-11d	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:086_R2_CTLA4BP-5x4-12c	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:087_R2_CTLA4BP-5x4-1f	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:088_R2_CTLA4BP-5x5-2e	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:089_R2_CTLA4BP-5x5-6e	(161)	ICSTSGGFPEPHLSWLENGEELNAISTTVSQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP
SEQ:090_R2_CTLA4BP-5x6-9d	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:091_R2_CTLA4BP-5x8-1f	(161)	ICSASGGFPEPHLFWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIRYGHLRVNQTFNWNTPKQEHFP
SEQ:092_R2_CTLA4BP-5x9-12c	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTASQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:222_ctla5x9d10	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTASQDPGTELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:223_ctla5x6f6	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:224_ctla5x5h12	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTDRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:225_ctla5x5c10	(161)	ICSTSGGFPEPHLFWLENGEELNAISTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP

Fig. 3E

Extracellular domain (ECD)

		161 … 240
SEQ:226_ctla5x3e8	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:227_ctla5x3c4	(161)	ICSTSGGFPEPRLAWMEDGEELNAINTTASQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:228_ctla5x3c3	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:229_ctla5x2h11	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTASQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:230_ctla5x2d7	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETGLYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:231_ctla5x2b7	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:232_ctla5x2b1 ns	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTGSSKLDFNMTTNHSFMCLIKYGHLRVNQTFSWNTPKQEHFP
SEQ:233_ctla5x1f1	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTASQDPETELYTVSSKLDFNMTANHSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:234_ctla5x1d7	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTASQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:235_ctla2x4g9	(161)	ICSTSGGFPEPRLAWMEDGEELNAISTTVSQDPGTELCTVSSKLDFNMTTNHSFMCLIRYGHLRVNQTFNWNTPKQEHFP
SEQ:236_ctla2x4a6	(161)	ICSTSGGFPEPHLFWLENGEELNAISTTVSQDPETELYAXSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:237_ctla2x2f3	(160)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:238_ctla2x2f12	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRANQTFNWNTPKQEHFP
SEQ:239_ctla2x1g8	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:240_ctla2x1f10	(161)	ICSTSGGFPEPRLAWMEDGEELNAINTTVSQDPGTELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:241_ctla2x1c9	(161)	ICSTSGGFPEPRLAWMEDGEELNAISTTASQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:242_ctla2x1h12	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:243_ctla2x1e2	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:244_ctla2x1c4	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTVSQDPGTELYAVSSKLDFNMTTNHNFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:245_ctla2x1b12	(161)	ICSTSGGFPEPRLAWMEDGEELNAINTTVSQDPETELYTVSSKLDFNMTANHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:246_ctla2x2f1	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTASQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:247_ctla5x4h1	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTASQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:248_ctla5x4a1	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:249_ctla5x2f3	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTASQDPETELYTVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:250_ctla5x2e12	(161)	ICSTSGGFPEPHLSWLENGEELNAISTTVSQDPGTELYAVSSKLDFNMTTNRSFVCLIKYGHLRVNQTFNWNTTKQEHFP
SEQ:251_ctla2x4h11	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP
SEQ:252_ctla2x3h2	(161)	ICSTPGGFPEPRLAWMEDGEELNAISTTVSQDPGTELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP
SEQ:286_CTLA4BP_Con	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFP

Fig. 3F

ECD → | ← TMD → | ← CD →

		241 ... 288
SEQ:278_Human_B7-1	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:069_R1_CTLA4BP-5	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:070_R1_CTLA4BP-7	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:071_R1_CTLA4BP-11	(241)	DNLLPSWAITLISVNGIFVICCLTHCFAPRCRERRRNERLRRESVHPV
SEQ:072_R1_CTLA4BP-13	(241)	DNLLPSWAITLISANGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
SEQ:073_R1_CTLA4BP-27	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNETLRRESVRPV
SEQ:074_R2_CTLA4BP-5x2-10c	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERR-NETLRRESVRPV
SEQ:075_R2_CTLA4BP-5x2-11d	(241)	DNLLPSWAITLISANGIFVICCLTYCFAPRCRERKSNETLRRESVRPV
SEQ:076_R2_CTLA4BP-5X2-12F	(241)	DNPLPSWAITLISANGIFVICCLTYCFAPRCRERRRNETLRRESVRPV
SEQ:077_R2_CTLA4BP-5x2-2g	(241)	DNLLPSWAITLISVNGIFVICCLTYRFAPRCRERKSNERLRRESVRPV
SEQ:078_R2_CTLA4BP-5x2-3c	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVCPV
SEQ:079_R2_CTLA4BP-5x2-4c	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVHPV
SEQ:080_R2_CTLA4BP-5x2-7b	(241)	DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:081_R2_CTLA4BP-5x2-8c	(241)	DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNERLRRESVHPV
SEQ:082_R2_CTLA4BP-5x3-10e	(241)	DNLLPSWAITLISANGIFVICCLTYCFAPRCRERKSNERLRRESVHPV
SEQ:083_R2_CTLA4BP-5x3-11b	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRSNERLRRESVRPV
SEQ:084_R2_CTLA4BP-5x3-6f	(241)	DNLLPSWAITLISANGIFVICCLAYCFAPGCRERKSNERLRRESVRPV
SEQ:085_R2_CTLA4BP-5x4-11d	(241)	DNLLPSWAITLISVNGIFVICCLTYRFAPRCRERKSNERLRRESVRPV
SEQ:086_R2_CTLA4BP-5x4-12c	(241)	DNLLPSWAITLISANGIFVICCLTYRFAPRCRERKSNETLRRESVRPV
SEQ:087_R2_CTLA4BP-5x4-1f	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVCPV
SEQ:088_R2_CTLA4BP-5x5-2e	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNETLRRESVRPV
SEQ:089_R2_CTLA4BP-5x5-6e	(241)	DNLLPSWAITLISANGIFVICCLTHCFAPRCRERKRNERLRRESVRPV
SEQ:090_R2_CTLA4BP-5x6-9d	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:091_R2_CTLA4BP-5x8-1f	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
SEQ:092_R2_CTLA4BP-5x9-12c	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
SEQ:222_ctla5x9d10	(241)	DNLLPSWAITLISVNGIFVICCLTHCFAPRCRERRRNERLRRESARPV
SEQ:223_ctla5x6f6	(241)	DNLLPSWAITLISANGIFVICCLTYRFAPRCRERRRNERLRRESVCPV
SEQ:224_ctla5x5h12	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNGRLRRESVRPV
SEQ:225_ctla5x5c10	(241)	DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVHPV

Fig. 3G

```
                  ECD →|←   TMD   →|←   CD   →
                       241                                              288
SEQ:226_ctla5x3e8  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPGCRERRRNERLRRESVCPV
SEQ:227_ctla5x3c4  (241) DNLFPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:228_ctla5x3c3  (241) DNLLPSWAITLISVNGIFVICCLTHCFAPRCRERRRNERLRRESVCPV
SEQ:229_ctla5x2h11 (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
SEQ:230_ctla5x2d7  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:231_ctla5x2b7  (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:232_ctla5x2b1 ns (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNETLRRESVRPVWGTKLKFKPXIS
SEQ:233_ctla5x1f1  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNETLRRESVRPV
SEQ:234_ctla5x1d7  (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERRRNERLRRESVHPV
SEQ:235_ctla2x4g9  (241) DNLLPSWAITLISVKGIFVICCLTYCFAPRGRERKSNGRLRRESVHPV
SEQ:236_ctla2x4a6  (241) DNLLPSWAITLISVNGIFVICCPTYCFAPRCRERRRNERLRRESVCPV
SEQ:237_ctla2x2f3  (240) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVCPV
SEQ:238_ctla2x2f12 (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:239_ctla2x1g8  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERKSNERLRRESVRPV
SEQ:240_ctla2x1f10 (241) DNLLPSWAITLISVNGISVICCLTYCFAPRCRERRRNERLRRESVCPV
SEQ:241_ctla2x1c9  (241) DNLLPSWAITLISVNGIFVICCLTHCFAPRCRERRRNERLRRESVCPV
SEQ:242_ctla2x1h12 (241) DNLLPSWAITLISANGIFVICCLTYCFAPRCRERKSNERLRRESVCPV
SEQ:243_ctla2x1e2  (241) DNLLPS-AITLISANGIFVICCLTYCFAPRCRERRRNERLRRESIHPV
SEQ:244_ctla2x1c4  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:245_ctla2x1b12 (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVCPV
SEQ:246_ctla2x2f1  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:247_ctla5x4h1  (241) NNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNETLRRESVHPV
SEQ:248_ctla5x4a1  (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:249_ctla5x2f3  (241) DNLLPSWAITLISANGIFVICCLTHCFAPRCRERKSNERLRRESVRPV
SEQ:250_ctla5x2e12 (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
SEQ:251_ctla2x4h11 (241) DNLLPSWAITLISVNGIFVICCLAYCFAPRCRGRRRNERLRRESVRPV
SEQ:252_ctla2x3h2  (241) DNLLPSWAITLISVKGIFVICCLTYCFAPRWRERKSNERLRRESVRPV
SEQ:286_CTLA4BP_Con (241) DNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV
```

Fig. 3H

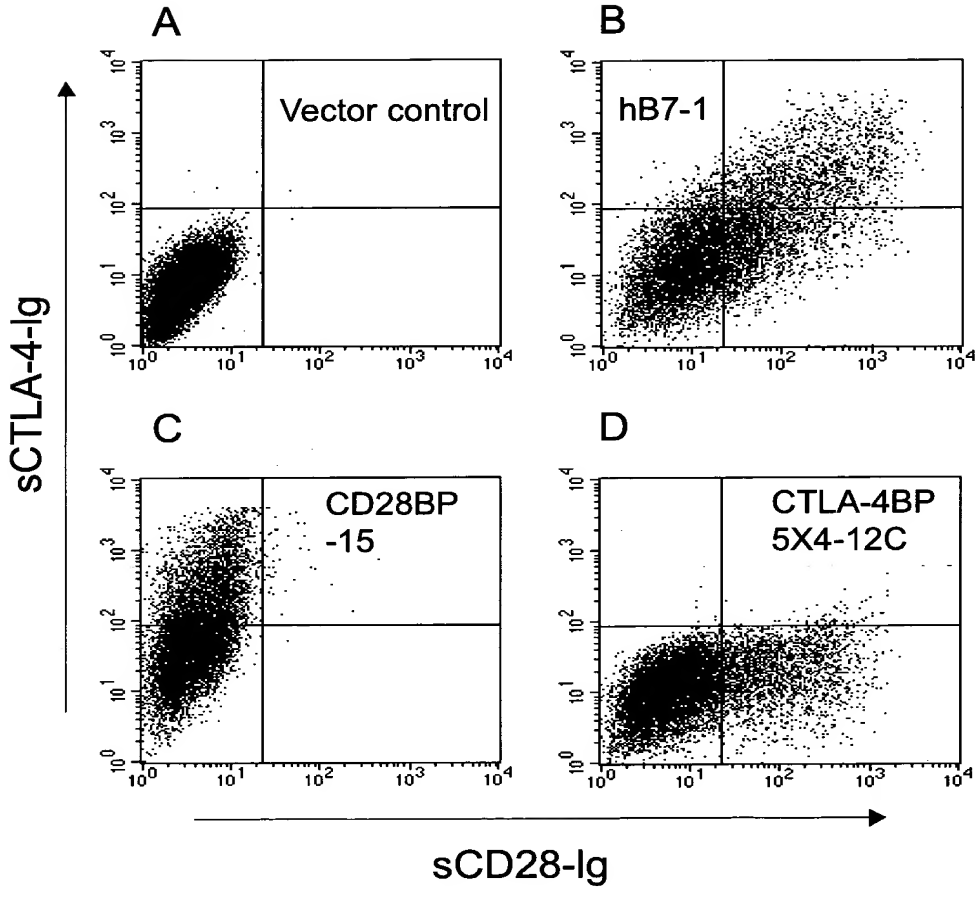

A
Vector control
B
hB7-1
C
CD28BP
-15
D
CTLA-4BP
5X4-12C
sCTLA-4-Ig
sCD28-Ig

Fig. 4

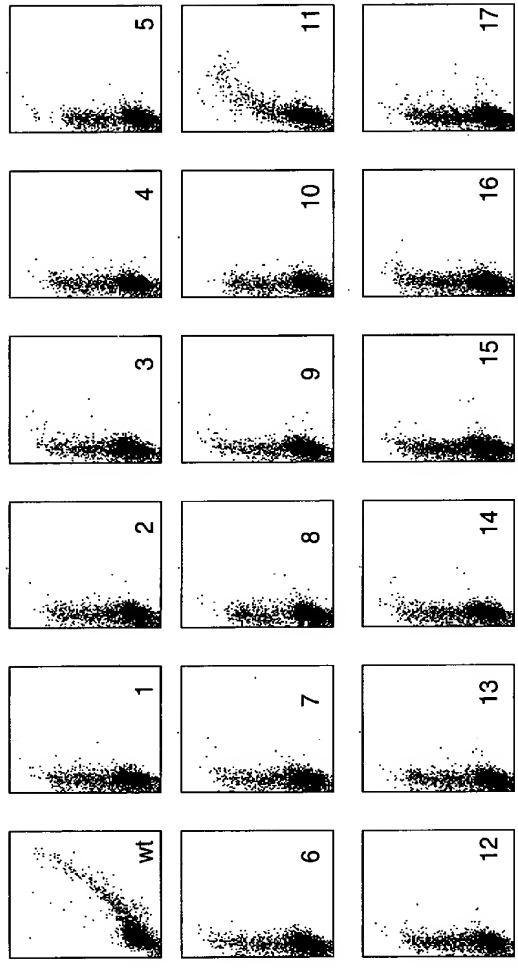


Fig. 5

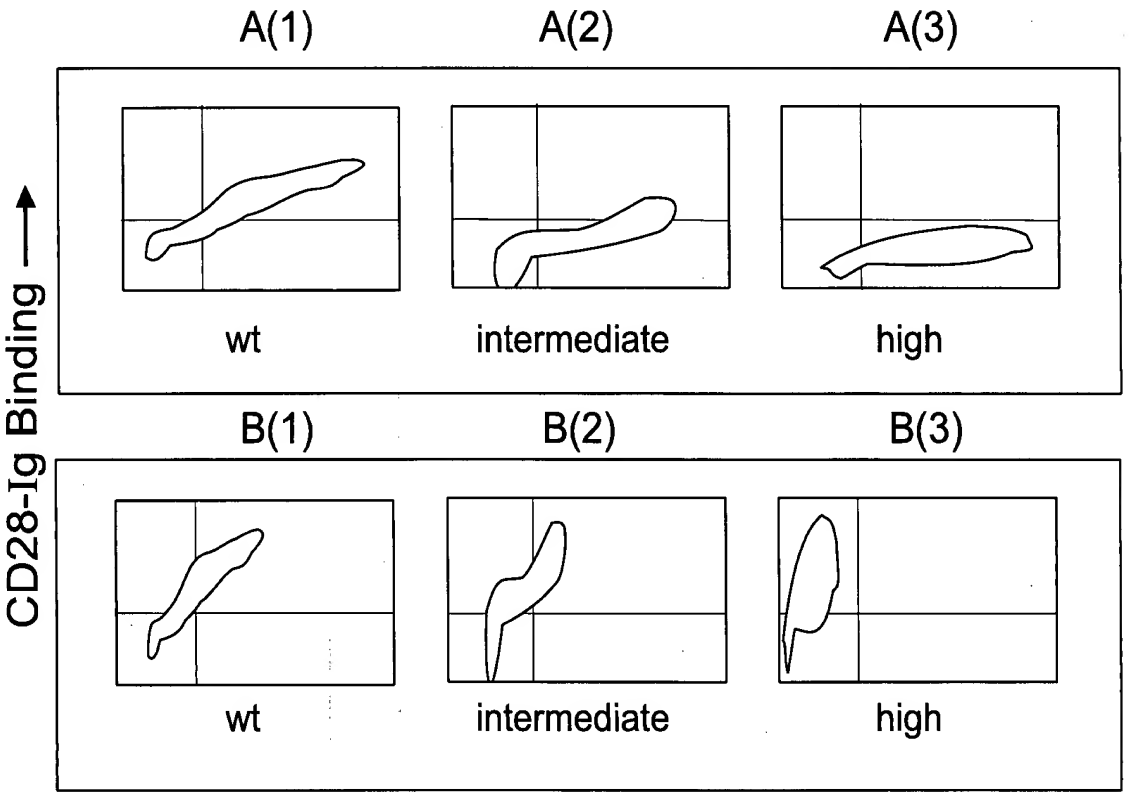

A(1)
A(2)
A(3)
wt
intermediate
high
B(1)
B(2)
B(3)
wt
intermediate
high
CD28-Ig Binding
CTLA-4-Ig Binding

Fig. 6

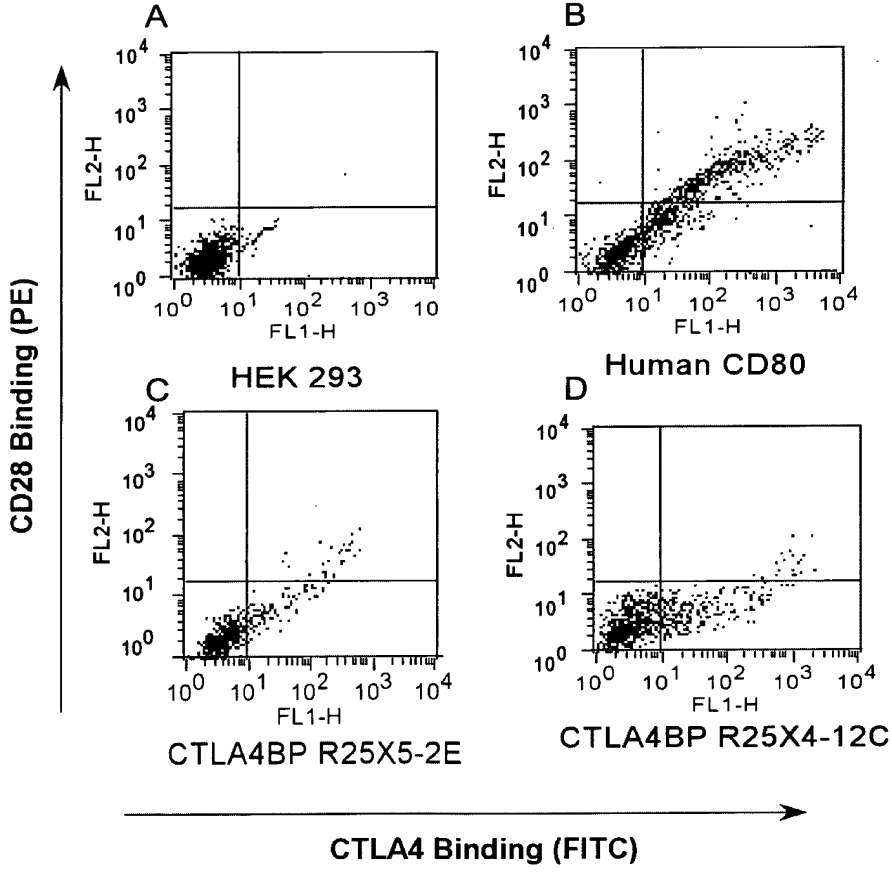

A
B
C
D
FL2-H
FL1-H
HEK 293
Human CD80
CTLA4BP R25X5-2E
CTLA4BP R25X4-12C
CD28 Binding (PE)
CTLA4 Binding (FITC)

Fig. 7A-D

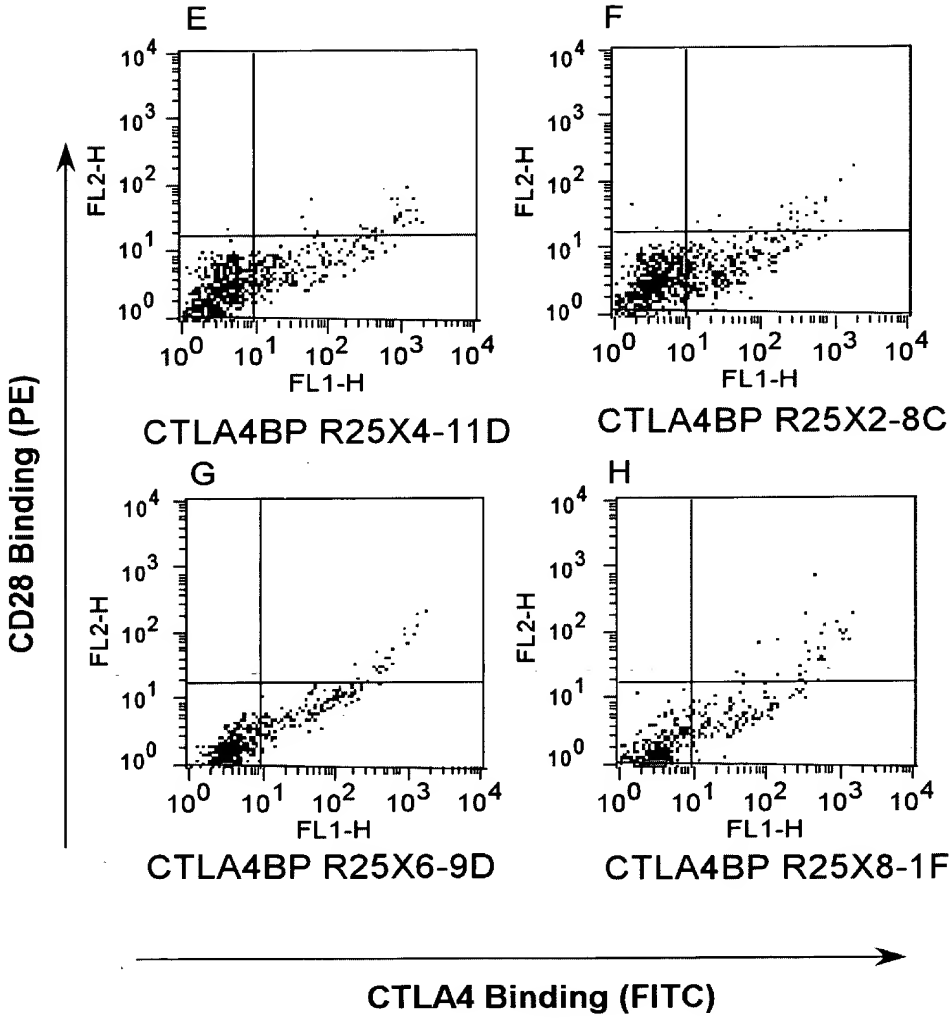

E
F
G
H
FL2-H
FL1-H
10^0 10^1 10^2 10^3 10^4
CTLA4BP R25X4-11D
CTLA4BP R25X2-8C
CTLA4BP R25X6-9D
CTLA4BP R25X8-1F
CD28 Binding (PE)
CTLA4 Binding (FITC)

Fig. 7E-H

Fig. 8A

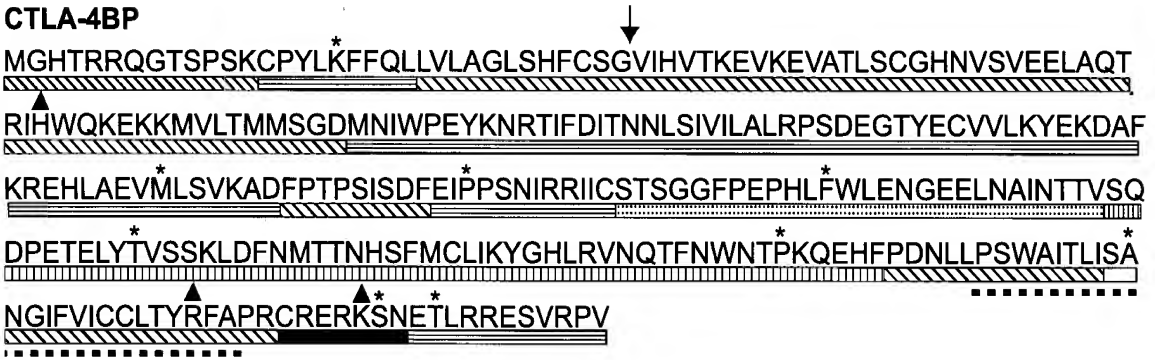


Fig. 8B

human
orangutan
rhesus
baboon
rhesus/baboon
cow
rabbit

Vector control
hB7-1
hB7-1-Flag
CD28BP-15
CD28BP-Flag
CTLA-4BP 5X4-12c

Fig. 9A

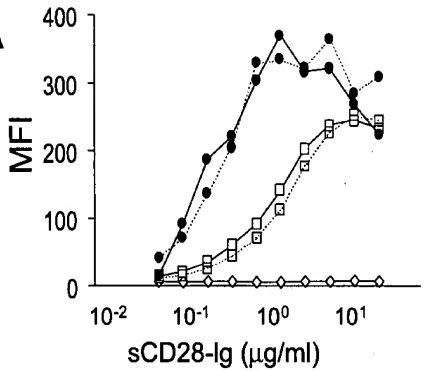


Fig. 9B

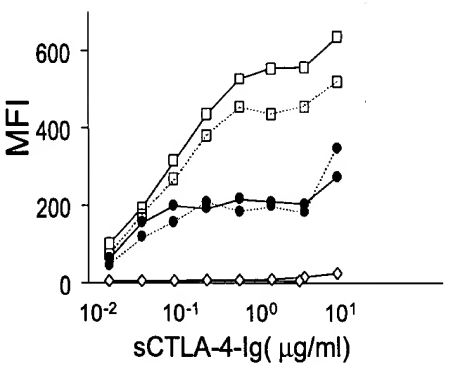


Fig. 9C

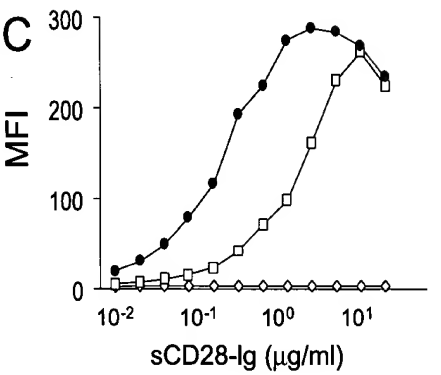


Fig. 9D

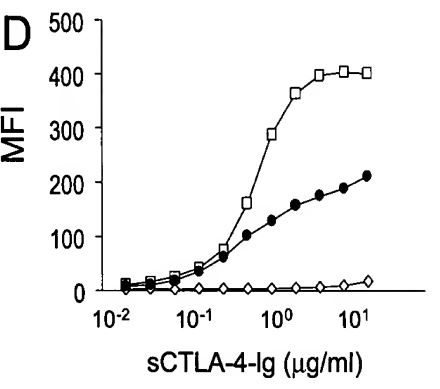


Fig. 9E

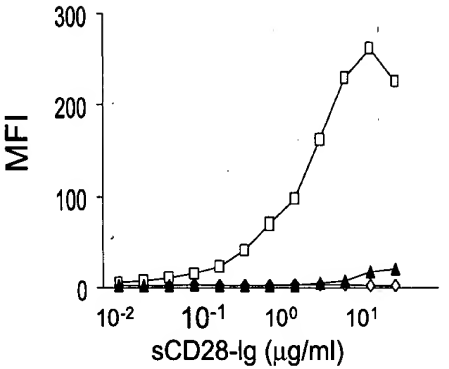


Fig. 9F

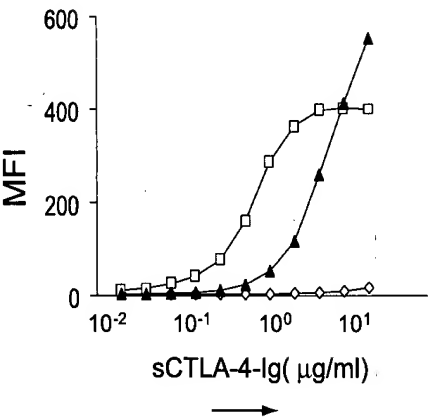


Fig. 9G

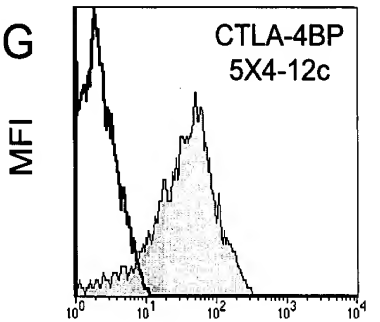


Fig. 9H

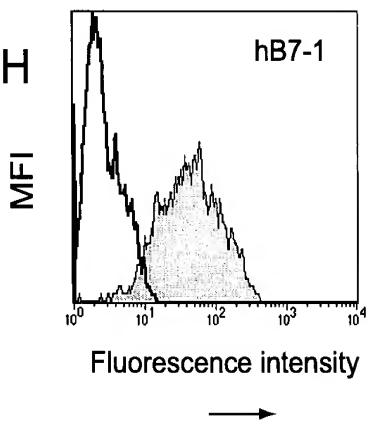


Fig. 10

Fig. 11A

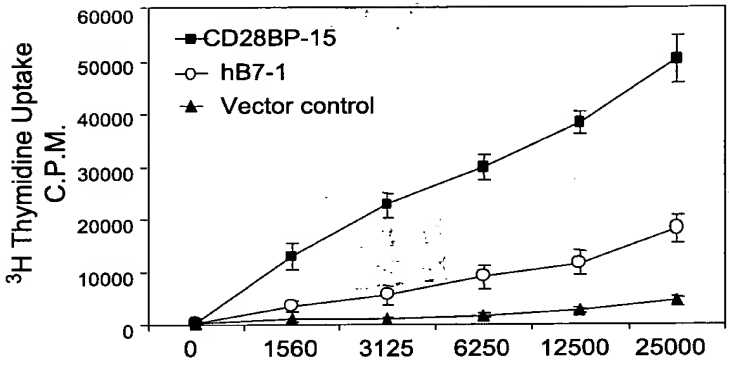


Fig. 11B

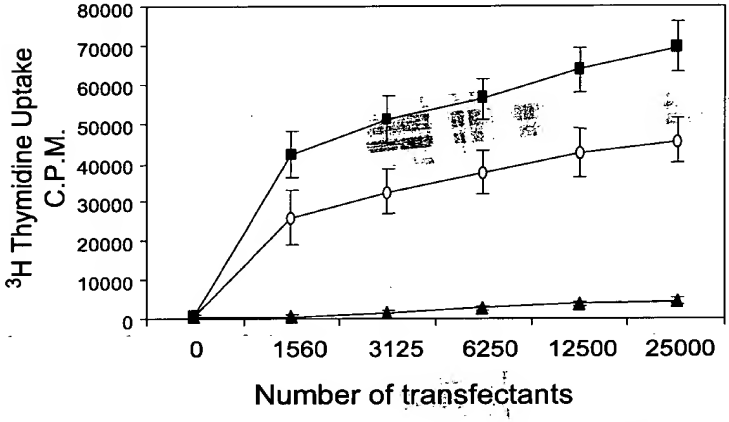
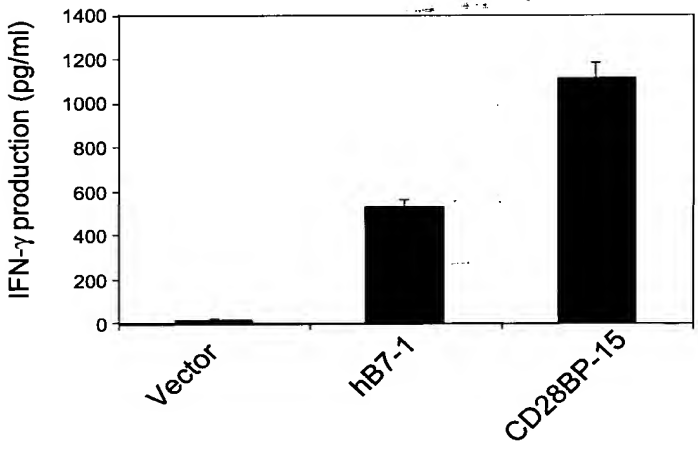


Fig. 11C



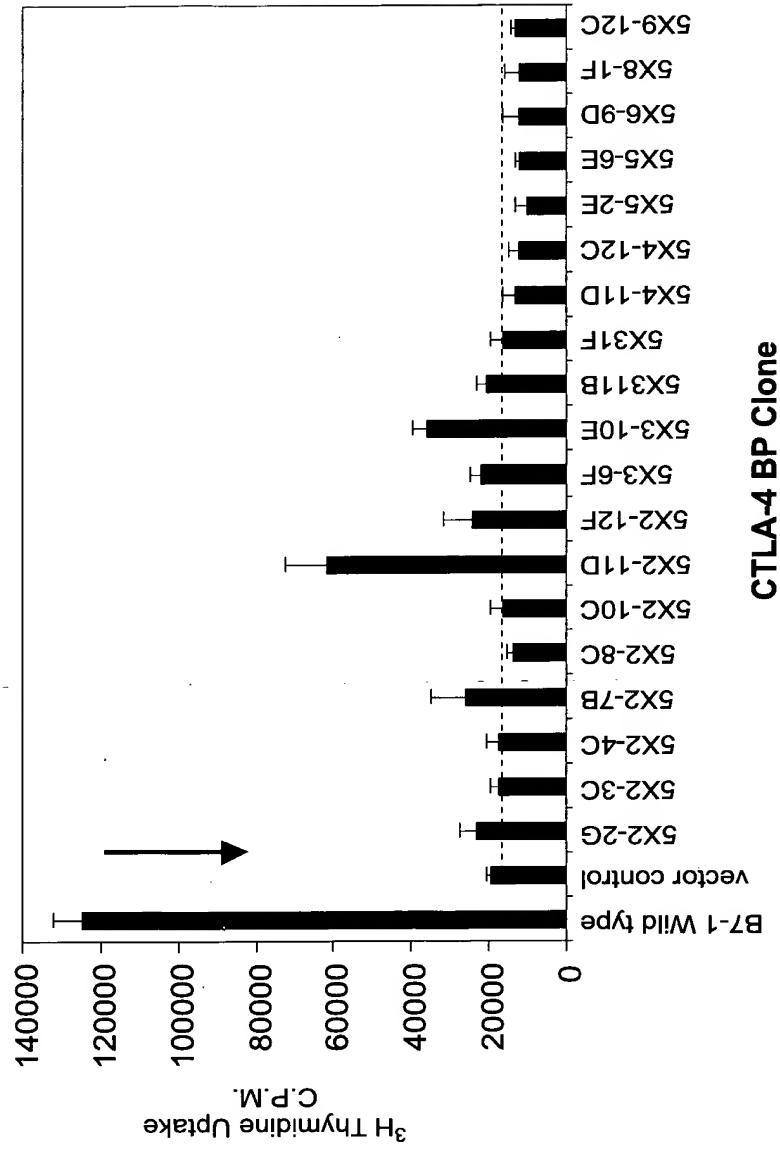

3H Thymidine Uptake
C.P.M.
140000
120000
100000
80000
60000
40000
20000
0
B7-1 Wild type
vector control
5X2-2G
5X2-3C
5X2-4C
5X2-7B
5X2-8C
5X2-10C
5X2-11D
5X2-12F
5X3-6F
5X3-10E
5X311B
5X31F
5X4-11D
5X4-12C
5X5-2E
5X5-6E
5X6-9D
5X8-1F
5X9-12C
CTLA-4 BP Clone

Fig. 12

Fig. 13A

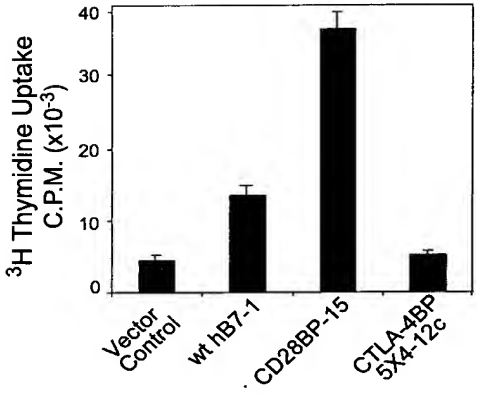


Fig. 13B

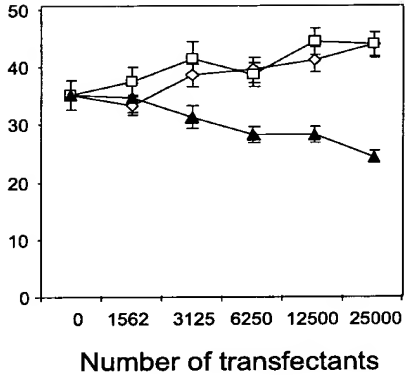


Fig. 13C

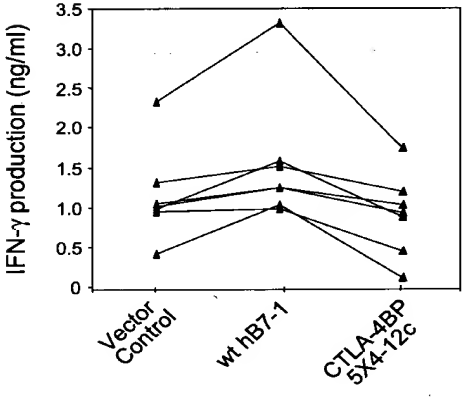


Fig. 13D

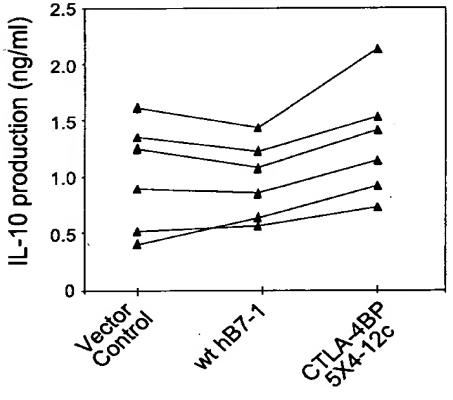


Fig. 14A

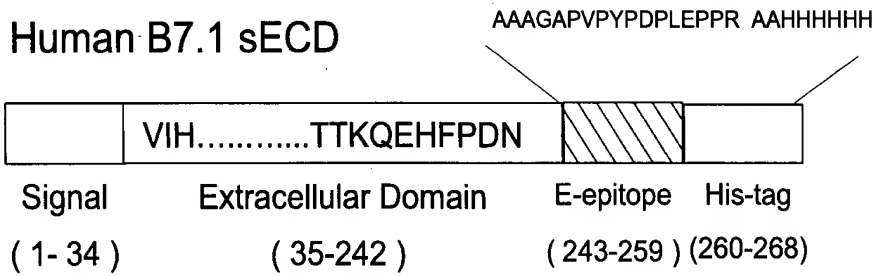
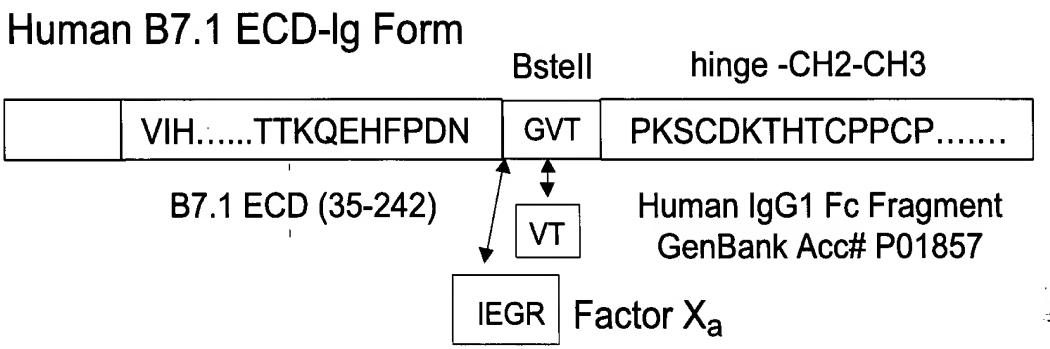


Fig. 14B



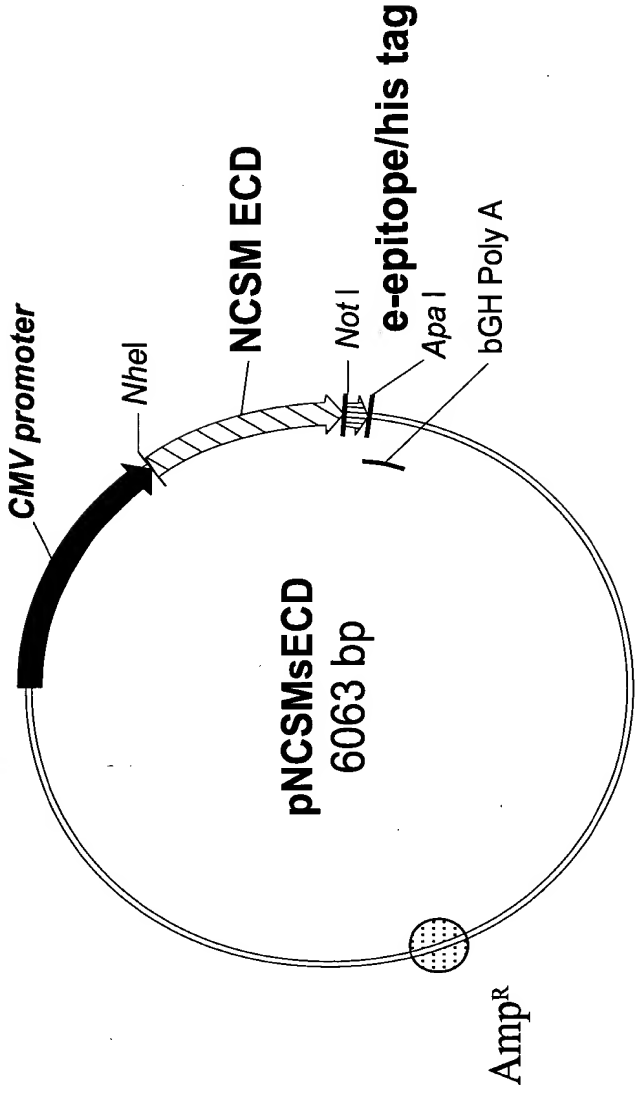

CMV promoter
NheI
NCSM ECD
NotI
e-epitope/his tag
ApaI
bGH Poly A
pNCSMsECD
6063 bp
Amp^R

Fig. 15

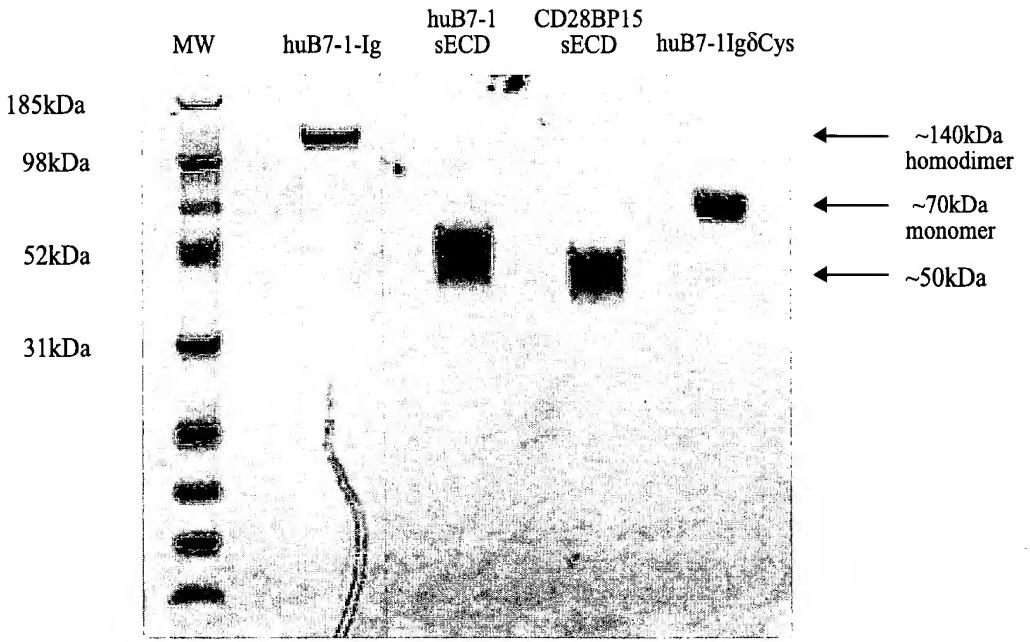

MW
huB7-1-Ig
huB7-1 sECD
CD28BP15 sECD
huB7-1IgδCys
185kDa
98kDa
52kDa
31kDa
~140kDa homodimer
~70kDa monomer
~50kDa

Fig. 16

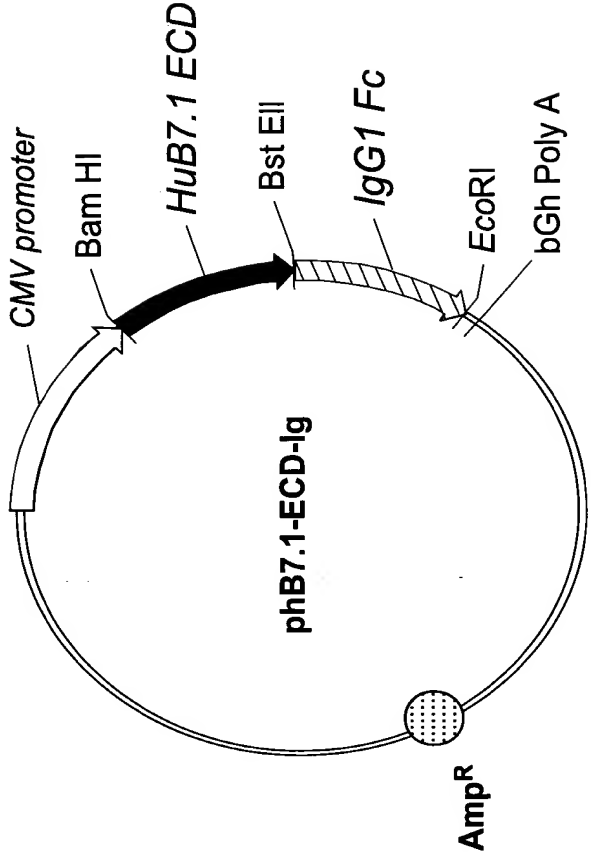

CMV promoter
Bam HI
HuB7.1 ECD
Bst EII
IgG1 Fc
EcoRI
bGh Poly A
phB7.1-ECD-Ig
AmpR

Fig. 17

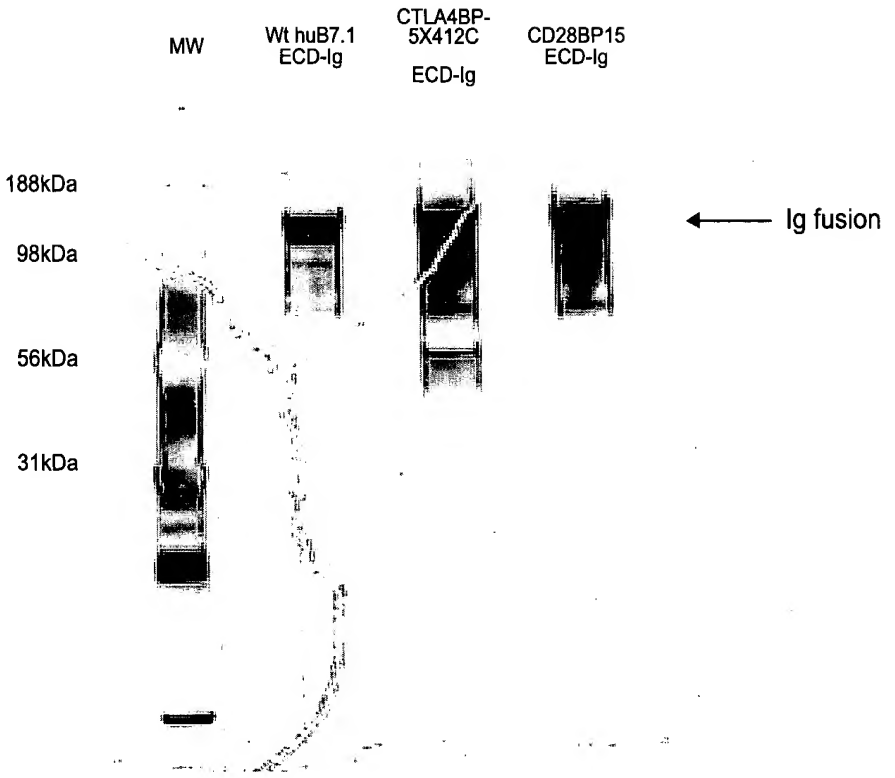

MW
Wt huB7.1 ECD-Ig
CTLA4BP-5X412C ECD-Ig
CD28BP15 ECD-Ig
188kDa
98kDa
56kDa
31kDa
Ig fusion

Fig. 18

Expression of CTLA-4BP-Ig and CD28BP-Ig Proteins

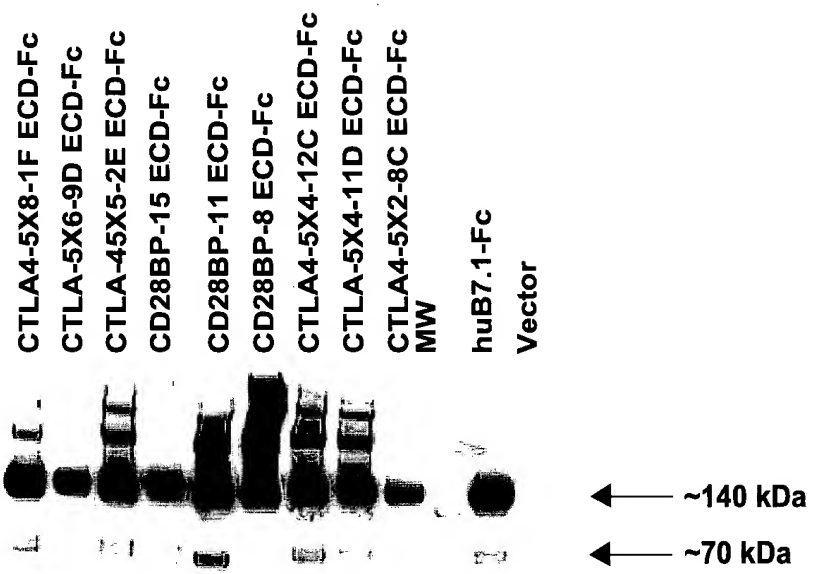


Fig. 19

Fig. 20A

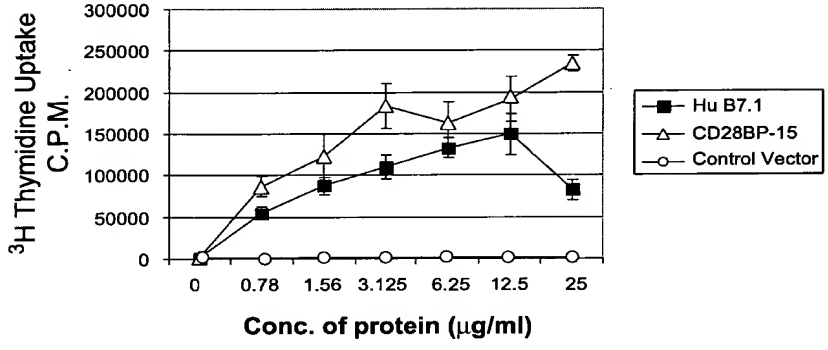


Fig. 20B

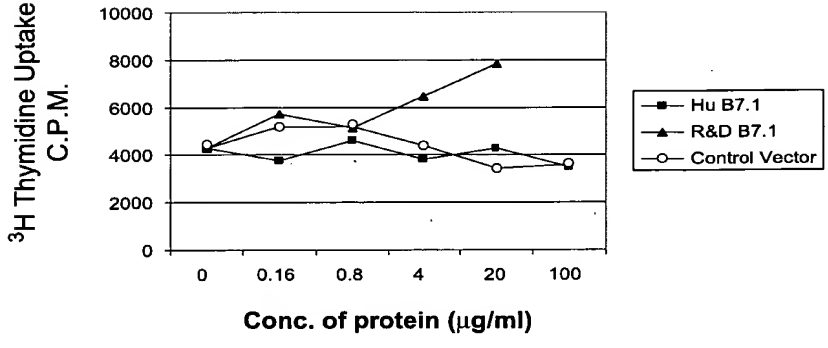


Fig. 20C

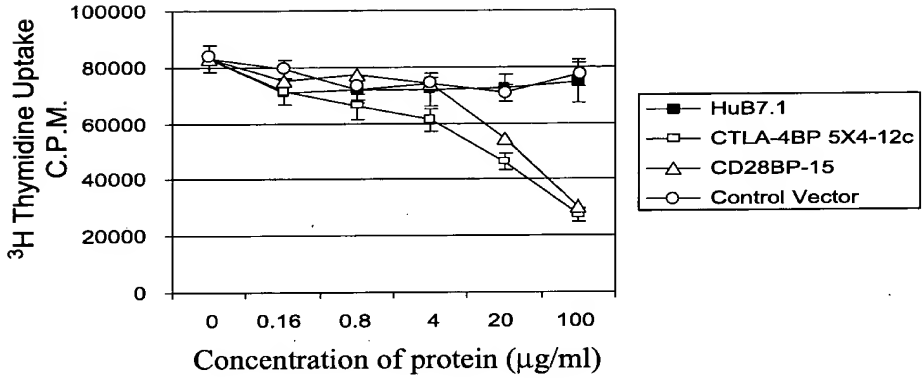
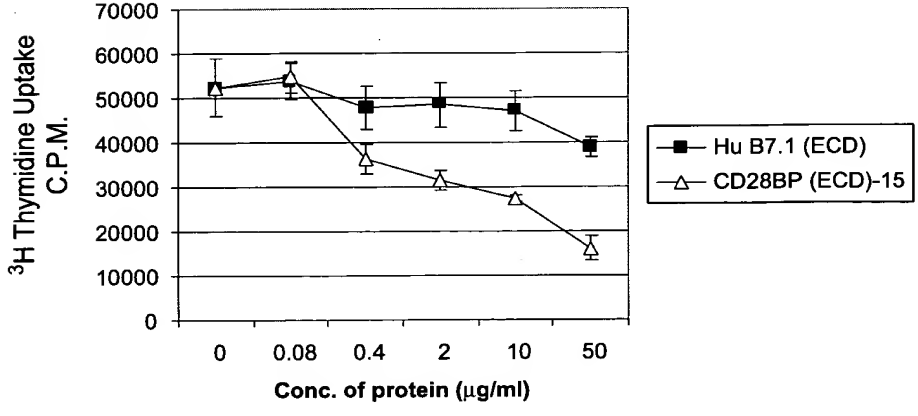


Fig. 20D



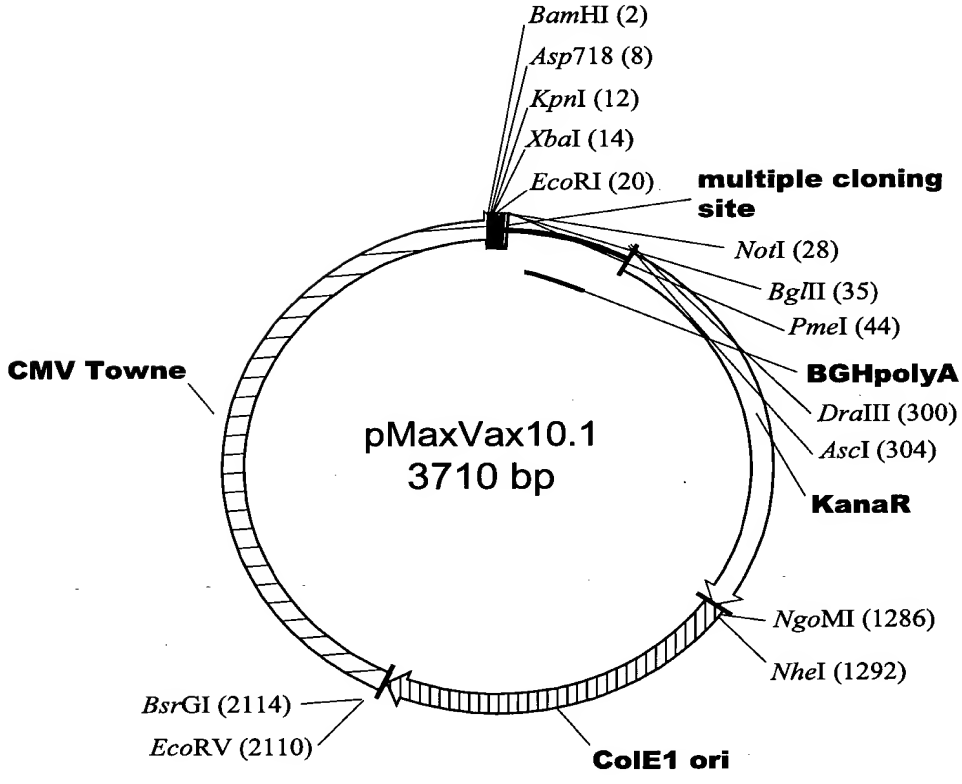


Fig. 21

Fig. 22A

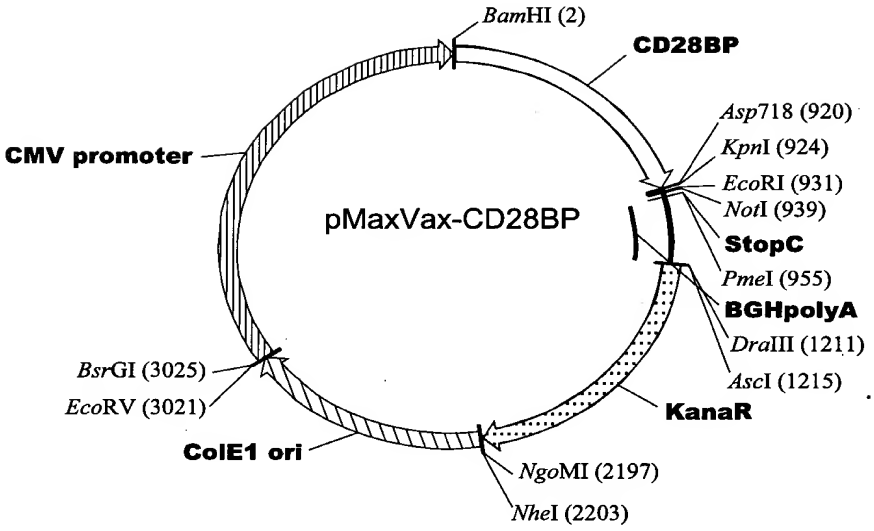


Fig. 22B